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In vivo tracking of 'color-coded' effector, natural and induced regulatory T cells in the allograft response

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Abstract

Here we present methods to longitudinally track islet allograft—infiltrating T cells in live mice by endoscopic confocal microscopy and to analyze circulating T cells by *in vivo* flow cytometry. We developed a new reporter mouse whose T cell subsets express distinct, 'color-coded' proteins enabling *in vivo* detection and identification of effector T cells (T_{eff} cells) and discrimination between natural and induced regulatory T cells (nT_{reg} and iT_{reg} cells). Using these tools, we observed marked differences in the T cell response in recipients receiving tolerance-inducing therapy (CD154-specific monoclonal antibody plus rapamycin) compared to untreated controls. These results establish real-time cell tracking as a powerful means to probe the dynamic cellular interplay mediating immunologic rejection or transplant tolerance.

Understanding the cellular immune response to transplanted tissue has a key role in developing strategies to improve transplant outcomes. Tissue biopsy is the standard method for accessing immune cell infiltration in the graft, but the method is both invasive and inadequate when temporal information is needed to characterize an immune reaction that progresses dynamically over time. Advances in molecular imaging techniques that combine cell labeling with the use of whole-body imaging modalities such as positron emission tomography, magnetic resonance imaging and bioluminescence imaging have led to promising approaches for tracking immune cells noninvasively *in vivo*[1–4], but these methods lack the sensitivity and spatial resolution to

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quantify events at the single-cell level. In addition, there is need to track multiple cell populations using labels that are not diluted by cell division.

Here we describe a real-time optical method for simultaneous tracking of multiple T cell subsets that are color-coded with distinct fluorescent reporters in a mouse model in which pancreatic islet transplants are placed beneath the renal capsule. As rejection occurs at 2 weeks in control untreated hosts, we track the T cell response for a period of 2 weeks after transplantation in both the circulatory compartment (by *in vivo* flow cytometry)[5] and within the allograft (by endoscopic confocal microscopy)[6]. *In vivo* flow cytometry allows noninvasive, continuous detection and quantification of fluorescently labeled cells in the circulation without the need to draw blood samples[5]. Endoscopic confocal microscopy enables minimally invasive imaging of internal organs with cellular definition by inserting a narrow-diameter endomicroscope through a small incision in the skin[6]. We show that repeated imaging of the islet allograft just beneath the renal capsule can be accomplished in the same mouse over the two-week period.

Islet transplantation is a promising clinical approach to restore insulin production and glucose regulation in patients with type 1 diabetes. The immune response to allogeneic islet transplants is $CD4^+$ T cell dependent[7–9], and includes both donor reactive, tissue-destructive T_{eff} cells and tissue-protective T_{reg} cells. The acquisition of transplant tolerance, a state in which the transplant is not rejected despite the cessation of immunosuppressive therapy, is associated with an alteration in the functional balance of T_{eff} and T_{reg} cells, as deduced in passive lymphocyte transfer experiments[10–12]. In addition, the pool of T_{reg} cells includes both nT_{reg} and iT_{reg} populations that arise during intrathymic T cell maturation or in the periphery when naive $CD4^+$ T cells are activated by antigen in the presence of transforming growth factor-β (TGF-β) and in the absence of interleukin-6 (IL-6) and IL-21, respectively[13,14]. The relative importance of iT_{reg} and nT_{reg} cells in the induction and maintenance of transplant tolerance is unclear because it has not been possible to readily distinguish these two T_{reg} subsets *in vivo*. Using our cell tracking technology, together with the color-coding scheme, we are now able to monitor not only T_{eff} and T_{reg} cells but also distinguish nT_{reg} from iT_{reg} cells in live mice to serially analyze the immune response to rejecting or tolerized major histocompatibility complex–mismatched islet transplants. As part of this study, we have tested the hypotheses that tolerance-inducing therapy will accelerate the rate and magnitude of conversion or accumulation of iT_{reg} cells from naive alloreactive T cells and lead to a profound increase in the number of allograft-infiltrating T_{reg} cells.

Results

Imaging and quantification of graft-infiltrating T cells

For islet transplantation, we first prepared C57BL/6 *Rag1*$^{-/-}$ recipient mice that lack lymphocytes by adoptive transfer of 1×10^6 nT_{reg} cells ($DsRed^-CD4^+GFP^+$) purified from C57BL/6 Foxp3-eGFP regulatory T cell reporter mice[13] together with 9×10^6 T_{eff} cells ($DsRed^+CD4^+GFP^-$) purified from C57BL/6 DsRed–knock-in mice (Fig. 1a). The proportion and number of transferred nT_{reg} and T_{eff} cells mimicked those present in normal wild-type mice (Supplementary Fig. 1a). On the next day, we placed a DBA/2 allogeneic islet graft underneath the left renal capsule (Supplementary Fig. 1a,b)[8]. One group of recipients received a tolerance-inducing protocol consisting of a 14-d course of CD154-specific monoclonal antibody (mAb) plus rapamycin. This regimen promotes conversion of antigen-activated naive T cells to iT_{reg} cells and donor-specific allograft tolerance[15]. In untreated hosts, all islet allografts were rejected by 14 d after transplantation (mean graft survival time, 12 d), whereas allografts in hosts receiving CD154-specific mAb plus rapamycin tolerizing treatment survived indefinitely (Fig. 1b).

We took a two-step approach to imaging the islet allograft. First, we verified our ability to identify and enumerate various T cell subsets at this location by intravital microscopy. Subsequently, we developed a minimally invasive method to accomplish these tasks through an endomicroscope.

Under appropriate conditions, $CD4^+Foxp3^-$ T_{eff} cells can convert into a $Foxp3^+$ phenotype, a characteristic of iT_{reg} cells[16,17]. To validate our color-coded system, we monitored *in vitro* conversion of T_{eff} to iT_{reg} cells by culturing purified T_{eff} cells collected from Ds-Red–knock-in mice ($DsRed^+CD4^+GFP^-$) with DBA/2-derived $B220^+$ splenic B cells in complete medium containing recombinant mouse TGF-β, IL-2 plus IL-4-specific and interferon-γ-specific antibodies[13,18]. Approximately 85% of T_{eff} cells cultured in these conditions acquired eGFP expression within 4 d (Supplementary Fig. 2), indicating their conversion to iT_{reg} cells.

Similarly, in our *in vivo* model, some $DsRed^+CD4^+GFP^-$ T_{eff} cells converted to $Foxp3^+GFP^+$ iT_{reg} cells after transplantation and become yellow (Fig. 1c). These yellow iT_{reg} cells ($DsRed^+CD4^+GFP^+$) could be readily distinguished from the green nT_{reg} cells ($DsRed^-CD4^+GFP^+$) that were originally transferred from the knock-in mice. Thus, we created a color-coded system in which T_{eff} cells were red, nT_{reg} cells were green and iT_{reg} cells were yellow (Fig. 1c). To verify that yellow cells were true double-positives and not an artifact created by overlapping red (T_{eff}) and green (nT_{reg}) cells within the allograft, we acquired Z-stack images in 1- to 2-μm steps (Supplementary Video 1) and generated reconstructed orthogonal slices (*xz* and *yz* planes) for analysis (Supplementary Fig. 3). Only red and green double-positive T cells that were negative in the third autofluorescence channel were identified as iT_{reg} cells (Supplementary Fig. 4).

Using intravital microscopy on days 1 and 4 after transplantation, very few T cells were identified within the islet allografts in either untreated hosts or hosts treated with CD154-specific mAb plus rapamycin (data not shown). On weeks 1 and 2 after transplantation, the densities of allograft-infiltrating T cells were much greater in untreated hosts than in treated hosts, with a predominant pattern of allograft infiltration by red T_{eff} cells (Fig. 2a). We analyzed only those images taken from the islet allograft sites, which can be readily distinguished from the surrounding kidney structure by their distinctive autofluorescence pattern (Supplementary Fig. 5). To our surprise, when we determined the absolute cell density of the three subsets of infiltrating T cells, the densities of allograft-infiltrating nT_{reg} and iT_{reg} cells were comparable in untreated and treated hosts at weeks 1 and 2 after transplantation (Fig. 2b,c). The prominent difference was the density of infiltrating T_{eff} cells, which was consistently and significantly higher in untreated hosts than in treated hosts at weeks 1 and 2 (Fig. 2d). As a result, the ratio of infiltrating nT_{reg} and iT_{reg} cells to infiltrating T_{eff} cells in treated hosts was much higher than in untreated hosts (Fig. 2e,f). Infiltration of the allograft by nT_{reg} cells was more prominent than infiltration by iT_{reg} cells.

To follow the time course of the T cell response in individual animals receiving islet transplants, we performed minimally invasive imaging with a 1.24-mm diameter endomicroscope inserted through a small incision in the skin[6]. This instrument allowed repeated imaging of the allograft site with minimal surgical manipulation and was able to resolve individual allograft infiltrating T cells (Fig. 3). By serially imaging the same mice at days 3, 5, 7, 10, 12 and 14 after islet transplantation, we obtained the kinetics of T cell infiltration in both the hosts treated with CD154-specific mAb plus rapamycin treated hosts and the untreated controls. Consistent with the intravital microscopy data, we observed a pronounced difference between the two hosts starting at day 7, dominated by the markedly increased number of red (T_{eff}) cells in the untreated allograft (Fig. 3).

Flow cytometry analysis of color-coded T cells

To test the accuracy of our color-coded system, we reconstituted C57BL/6 CD45.2$^+$ *Rag1*$^{-/-}$ mice with 1×10^6 CD45.2$^+$DsRed$^-$CD4$^+$ GFP$^+$ nT_{reg} cells from knock-in mice and 9×10^6 CD45.1$^+$ DsRed$^+$CD4$^+$GFP$^-$ $_{eff}$ cells from CD45.1$^+$ CD45.2$^+$ (F_1 generation) DsRed–knock-in mice. Islet allografts were performed exactly as described previously[8]. We analyzed spleen samples from both untreated recipients and recipients treated with CD154-specific mAb plus rapamycin 2 weeks after transplantation (Table 1). In untreated hosts, 98.9% of all CD4$^+$DsRed$^+$ T cells were CD4$^+$CD45.1$^+$, whereas in treated hosts the percentage was 96.2%. Similarly, 97.5% and 88.5% of CD4$^+$CD45.1$^+$ cells were CD4$^+$DsRed$^+$ in untreated and treated hosts, respectively. To identify false positives, we determined the percentages of CD4$^+$CD45.1$^+$ cells in the CD4$^+$DsRed$^-$ population and CD4$^+$DsRed$^+$ cells in CD4$^+$CD45.1$^-$ population. In the untreated hosts, the percentages were 2.4% and 1.1%, respectively, whereas the percentages in the treated hosts were 8.3% and 2.6%, respectively. Thus, the detection of cell subsets via analysis of cell surface CD45 isoform expression as an independent marker validated the accuracy of the color-coded system.

We used *ex vivo* flow cytometry analysis to determine the number, distribution and ratios of red T_{eff} green nT_{reg} and yellow iT_{reg} cells in the allograft-draining lymph node at 2 weeks after islet transplantation from both untreated hosts and hosts treated with CD154-specific mAb plus rapamycin (Supplementary Table 1). The ratio of iT_{reg} to T_{eff} cells in the allograft was consistently elevated in treated hosts at 1 week and 2 weeks after transplantation and in the draining lymph node at 2 weeks after transplantation (Supplementary Table 1). The ratio of nT_{reg} to T_{eff} cells in the allograft was consistently elevated in treated hosts compared to untreated hosts at 1 week and 2 weeks after transplantation, but, in the draining lymph node at 2 weeks, the difference between treated and untreated hosts disappeared (Supplementary Table 1). As might be anticipated, the ratios were far more variable in spleen and nonallograft-draining peripheral lymph node, sites that are distant from the transplant (data not shown). Nonetheless, the ratios of iT_{reg} cells to T_{eff} cells and nT_{reg} cells to T_{eff} cells were consistently higher in hosts treated with CD154-specific mAb plus rapamycin compared to untreated hosts in spleen and peripheral nondraining lymph node (data not shown).

Monitoring circulating T cells by *in vivo* flow cytometry

To determine whether these T cell subtypes can be detected in the peripheral blood, we serially monitored the number of fluorescent cells flowing through an ear artery by *in vivo* flow cytometry. In both hosts treated with CD154-specific mAb plus rapamycin and untreated hosts, we detected circulating T_{eff} and nT_{reg} cells by 2 d after transplantation, and we detected iT_{reg} cells by 4 d after transplantation (Fig. 4a). The number of circulating T cells increased from day 2 to week 1 after transplantation, with T_{eff} cells greatly outnumbering both T_{reg} cell populations (Fig. 4b), but we did not identify any statistically significant difference between the two groups. Circulating T_{eff} cells were significantly more abundant in untreated hosts than in hosts treated with CD154-specific mAb plus rapamycin at week 2, at which time the allograft was undergoing rejection in the untreated control mice (Fig. 1b). In contrast, there was still no statistical difference in the numbers of T_{reg} cells identified in these two groups. The ratio of T_{reg} to T_{eff} cells in the circulation was significantly higher in hosts treated with CD154-specific mAb plus rapamycin as compared to untreated hosts at weeks 1 and 2 after transplantation (Fig. 4c).

Discussion

Analysis of the T cell-dependent immune response to allogeneic tissues has been hampered by the inability to serially identify iT_{reg} and nT_{reg} cell subsets in a living host. The recent development of T_{reg} cell reporter GFP knock-in mice has provided a powerful means to identify

the Foxp3$^+$ T_{reg} cell population, but *Foxp3* promoter–driven GFP is expressed by both nT_{reg} and iT_{reg} cells[13,19].

We have now devised a means to serially analyze the allograft response through application of a unique tricolor-coded reporter system that enables discrimination not only between T_{eff} and T_{reg} cells but also between nT_{reg} and iT_{reg} cells. By placing islet transplants beneath the renal capsule, allograft-infiltrating T cells can be serially analyzed by endoscopic microscopy over time in the same host. Concurrently, subsets of circulating T cells can be quantified in a peripheral artery of the same living host by *in vivo* flow cytometry, without the need to draw blood samples. Compared to previous studies using traditional immunohistochemistry or standard flow cytometry that provide static 'snapshots' of T cell infiltration during allograft response[20,21], our technology allows a more complete, serial characterization of the immune response by dynamic tracking of various T cell populations both in the circulatory compartment and at the graft site of the same living host over a course of days to weeks.

With these tools, we have analyzed the T cell response to islet allografts in untreated rejecting recipients and in recipients given a transplant tolerance–inducing regimen[22,23]. The fate of the allograft, either rejection or tolerance, depends upon the functional balance of alloreactive graft–protecting T_{reg} cells to alloreactive graft–destroying T_{eff} cells[11,24–26]. In the absence of a favorable change in balance of T_{reg} to T_{eff} cells, the former cells are unable to restrain the latter cells from rejecting the transplant. Although it is known that tolerance cannot readily be induced in major histocompatibility complex–mismatched transplants in the absence of apoptosis of alloreactive T cells[22,23], the precise numeric change in the balance between T_{eff} and T_{reg} cells is not known. Moreover, it is not known whether nT_{reg} or iT_{reg} cells predominate in the graft-protective response noted in tolerized hosts. In fact, it is expected but not actually known whether these T_{reg} cell populations expand or accumulate more markedly in tolerized compared to rejecting recipients. Through the implementation of serial microendoscopy, we observed an expected increase in the of iT_{reg} to T_{eff} ratio among CD4$^+$ T cells that infiltrate the transplant in tolerized hosts as compared to rejecting hosts. Although we anticipated a massive increase in conversion or accumulation of iT_{reg} cells in tolerized as compared to rejecting hosts, this hypothesis is not supported by our data, at least within the context of our passive transfer model. We did not observe a striking numeric increase in allograft-infiltrating iT_{reg} cells in tolerized hosts compared to untreated hosts. Also unanticipated was our observation that infiltration of the allograft by nT_{reg} cells predominated over infiltration by iT_{reg} cells. The most dramatic change in the response of tolerized versus rejecting recipients was the pronounced decrease in tempo and magnitude of allograft infiltration by T_{eff} cells, a change that overshadows any change in nT_{reg} or iT_{reg} populations in tolerized hosts. As a consequence, the proportion of allograft-infiltrating T_{reg} to T_{eff} cells is very markedly enhanced in tolerized hosts. These data corroborate and give insight into the key role of reduction of the pool of donor-reactive effector T cells as a precondition for tolerance induction[22,23]. A reduction in allograft infiltration by graft destructive effector, but not regulatory, T cells enables T_{reg} cells to restrain the ability of the diminished cohort of allograft-infiltrating T_{eff} cells to reject the transplant.

In keeping with the appearance of T_{reg} cells within the allograft, we detected both nT_{reg} and iT_{reg} cells in the peripheral blood by *in vivo* flow cytometry. Indeed, we detected all three T cell subtypes in the circulation of both rejecting and tolerized hosts, days before they were discerned infiltrating the allografts. In agreement with the imaging data, we did not detect massive conversion of iT_{reg} cells in tolerized hosts, even though the technology is clearly able to detect converted iT_{reg} cells in the circulation, thereby providing unequivocal evidence of the capacity of naive T cells to convert to the Foxp3$^+$ phenotype *in vivo*. Detection of circulating iT_{reg} cells as early as day 4 after transplantation suggests that iT_{reg} conversion is an inevitable early event in the allograft response. Notably, the circulating T_{reg} to T_{eff} ratio is consistently

and substantially higher in tolerized compared to rejecting hosts, raising the possibility that peripheral blood analysis can be used as an early diagnostic method, enabling more timely and effective therapy to improve transplantation outcomes.

The serial application of endoscopic confocal microscopy and *in vivo* flow cytometry to a color-coded T cell reporter system has enabled a clearer understanding of both quantitative and qualitative characteristics of the $CD4^+$ T cell response to allografts in rejecting and tolerized hosts. Indeed, the hypothesis that we held concerning the ability of co-stimulation blockade–based transplant tolerizing therapy to enable massive expansion of allograft-infiltrating T_{reg} cells, especially iT_{reg} cells, was proven incorrect. Although we have studied the allograft response in a system based on transfer of lymphocytes into lymphopenic hosts, albeit in a manner that minimizes homeostatic proliferation, we believe application of these methods to other models will enable further progress in a meticulous dissection of the cellular and molecular basis of the allograft response. Our studies also point to a clear need for further refinement of the endoscopic imaging technique, so that serial monitoring of the cellular response in the allograft-draining lymph node with minimal invasion will become possible.

Methods

Methods and any associated references are available in the online version of the paper at http://www.nature.com/naturemedicine/.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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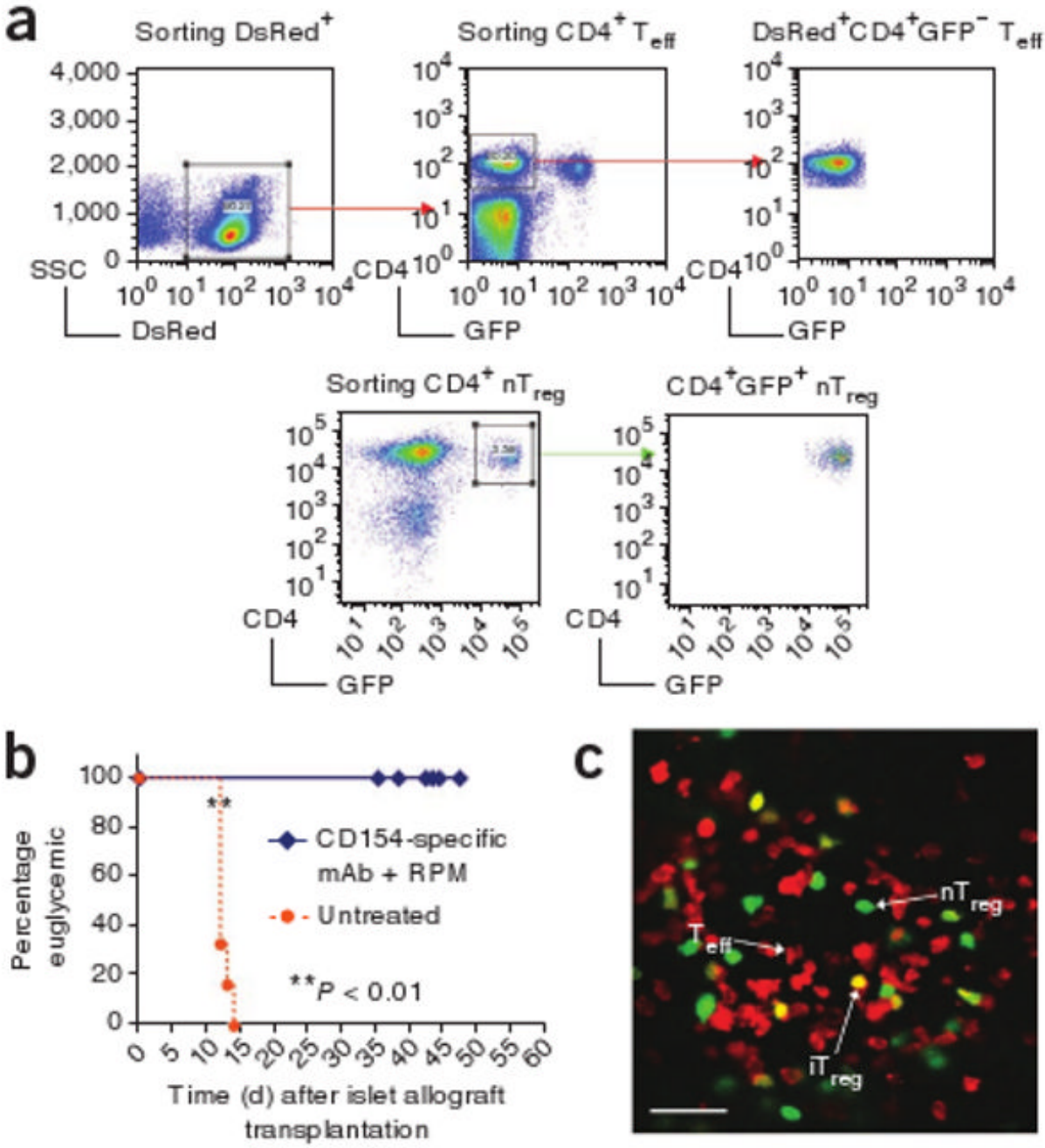

Figure 1.

In vivo imaging of color-coded T cells. (**a**) FACS sorting of DsRed^{+}CD4^{+}GFP^{-} red T_{eff} cells from DsRed–knock-in mice and CD4+GFP+ green nT_{reg} cells from the original knock-in mice. (**b**) Graft survival curves of mice treated with CD154-specific mAb plus rapamycin and untreated rejecting controls. The difference in the survival curves is significant, as calculated by either log-rank (Mantel-Cox) ($P = 0.0004$) or Gehan-Breslow-Wilcoxon ($P = 0.0012$) tests. (**c**) Representative image of allograft-infiltrating nT_{reg} (green), T_{eff} (red) and iT_{reg} cells (yellow) acquired by intravital microscopy. Scale bar, 50 μm.

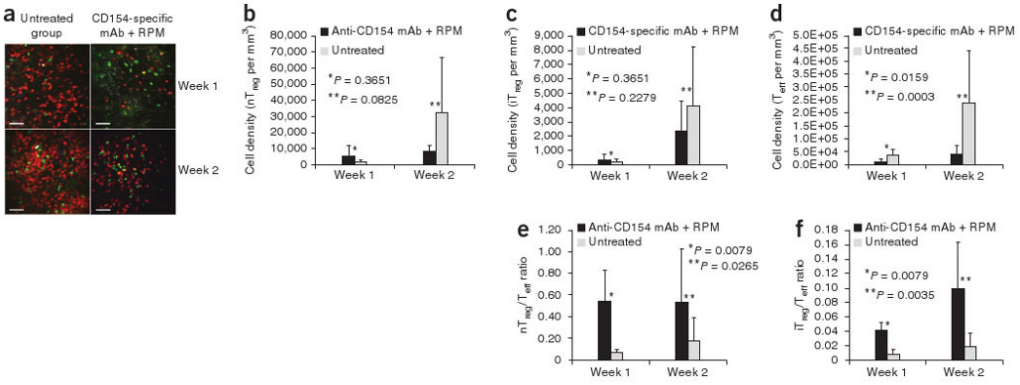

Figure 2.

Analysis of infiltrating T cells within islet allografts. (**a**) Representative intravital microscopy images showing T cell infiltration within islet allografts in untreated hosts and hosts treated with CD154-specific mAb plus rapamycin on week 1 and week 2 after transplantation. Scale bar, 100 μm. (**b**–**d**) Summary of cell density of islet allograft–infiltrating nT_{reg} (**b**), iT_{reg} (**c**) and T_{eff} (**d**) cells, as detected by intravital imaging. (**e,f**) Summary of the ratios of islet allograft–infiltrating nT_{reg} to T_{eff} (**e**) and iT_{reg} to T_{eff} (**f**) cells, as detected by intravital imaging. Error bars represent means ± s.d.

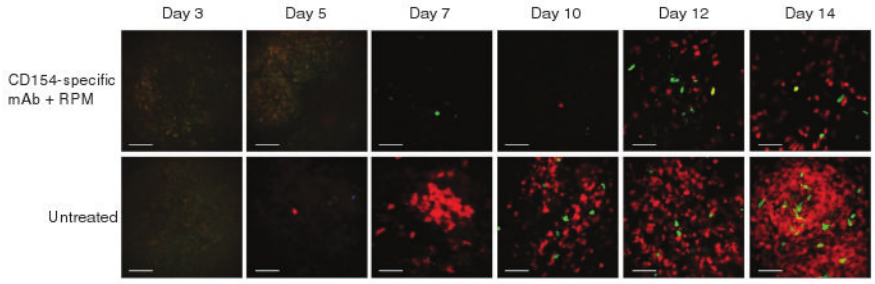

Figure 3.

Serial endomicroscopy of infiltrating T cells within islet allografts. Representative endomicroscopy images within islet allografts on days 3, 5, 7, 10, 12 and 14 after transplantation in untreated hosts and hosts treated with CD154-specific mAb plus rapamycin. Each row of images is from the same mouse at the given time points. Infiltrating nT_{reg} (green), T_{eff} (red) and iT_{reg} cells (green + red) accumulate in the allograft over time. Scale bar, 50 μm.

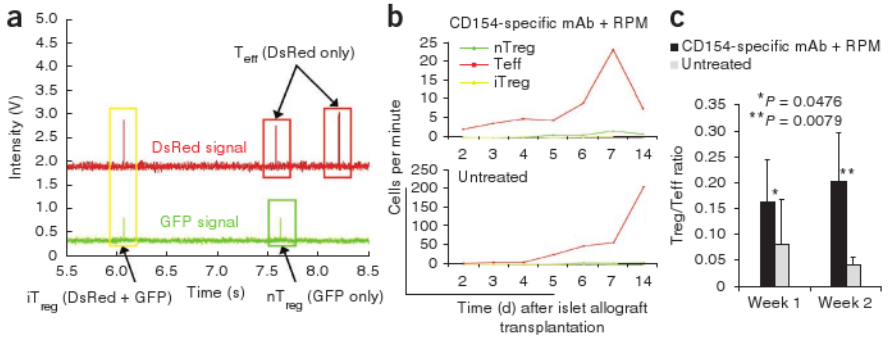

Figure 4.

Detection of nT_{reg}, T_{eff} and iT_{reg} cells by *in vivo* flow cytometry in the peripheral blood. (**a**) A representative *in vivo* flow cytometry trace showing the identification of single positive nT_{reg} (green box), T_{eff} (red boxes) and double-positive iT_{reg} (yellow box) cells. The second peak in the DsRed channel occurred about 45 ms before the second peak in the GFP channel. As this time difference was greater than the uncertainty of the measurements, these two peaks were distinguished as separate cells and not a double-positive iT_{reg} cell. (**b**) *In vivo* flow cytometry showing T_{eff} (red), nT_{reg} (green) and iT_{reg} cells (yellow) in the peripheral blood. There is a ten-fold difference in scale between mice treated with CD154-specific mAb plus rapamycin and untreated mice. Each curve represents serial analysis of the same blood vessel of the same animal. (**c**) Summary of the ratio of circulating T_{reg} to T_{eff} cells, as detected by *in vivo* flow cytometry. Error bars represent means ± s.d.

Table 1
External validation of DsRed with the congenic marker CD45.1 by *ex vivo* flow cytometry

$CD45.1^+$ in $DsRed^+$	Untreated	98.9%
population	CD154-specific mAb plus rapamycin	96.2%
$DsRed^+$ in $CD45.1^+$	Untreated	97.5%
population	CD154-specific mAb plus rapamycin	88.5%
$CD45.1^+$ in $DsRed^-$	Untreated	2.4%
population	CD154-specific mAb plus rapamycin	8.3%
$DsRed^+$ in $CD45.1^-$	Untreated	1.1%
population	CD154-specific mAb plus rapamycin	2.6%

The correlation of the CD45.1 congenic marker with DsRed was calculated from spleen samples from the untreated mice and mice treated with CD154-specific mAb plus rapamycin on week 2 after transplantation by *ex vivo* flow cytometry on the basis of the percentage of $CD4^+CD45.1^+$ cells in the $CD4^+DsRed^+$ population and on the percentage of $CD4^+DsRed^+$ cells in the $CD4^+CD45.1^+$ population. False positives were calculated as the percentages of $CD4^+CD45.1^+$ cells in the $CD4^+DsRed^-$ population and $DsRed^+$ cells in the $CD4^+CD45.1^-$ population.